GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: November 5, 2001, 14:28:35 ; Search time 5173.87 Seconds
(without alignments)
4834.167 Million cell updates/sec

Title: US-09-593-316-3
Perfect score: 1617
Sequence: 1 ccgqqqqccqqqcccqaqctg..... ..atttqagaqaqqtattattct 1617

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: qb_ba1:*
2: qb_ba2:*
3: qb_ba3:*
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5: qb_in2:*
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94: qb_ro1:*
95: qb_ro2:*
96: qb_in4:*
97: qb_pr10:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1617	100.0	1828	7	BOVGSTA	J04989 Bovine alph
2	1617	100.0	1828	9	AR066334	AR066334 Sequence
3	1005	62.2	3684	7	AF221508	AF221508 Sus scrof
4	968.6	59.9	3640	7	AF221509	AF221509 Sus scrof
5	944.4	58.4	1412	9	AR066333	AR066333 Sequence
6	893.6	55.3	1269	7	PIGGGTA	L36152 Sus scrofa
7	866	53.6	1128	9	A69344	A69344 Sequence 1
8	866	53.6	1128	9	A72021	A72021 Sequence 1

9	824.6	51.0	1181	97	S71333	S71333 alpha 1,3 g
10	819.4	50.7	1443	7	P16A13G	L36535 Sus scrofa
11	819.4	50.7	1423	9	AR048516	AR048516 Sequence
12	792	49.0	1092	9	A69346	A69346 Sequence 3
13	792	49.0	1092	9	A72023	A72023 Sequence 3
14	778.6	48.2	1065	9	A69348	A69348 Sequence 5
15	778.6	48.2	1065	9	A72025	A72025 Sequence 5
16	741.8	45.9	1029	9	A69350	A69350 Sequence 7
17	741.8	45.9	1029	9	A72027	A72027 Sequence 7
18	711.6	44.0	3450	9	AR066335	AR066335 Sequence
19	711.6	44.0	3450	94	MUSGLYENS	M85154 M.musculus
20	704.8	43.6	1885	97	HUMIGF2	M60263 Human alpha
21	704.8	43.6	194800	62	AC012485	AC012485 Homo sapi
22	704.8	43.5	1353	9	AR048515	AR048515 Sequence
c 23	697	43.1	253103	62	AC012518	AC012518 Homo sapi
24	642.4	39.7	1500	9	AR075307	AR075307 Sequence
25	642.4	39.7	1500	10	134188	134188 Sequence 3
26	642.4	39.7	1500	94	MUSGALA	M26925 Mouse galac
27	648.8	39.5	1053	89	AF197007	AF197007 Pan troql
28	641.8	39.1	153814	75	AC078879	AC078879 Homo sapi
29	610.4	37.7	1048	89	AF196986	AF196986 Homo sapi
30	606.2	37.5	4900	7	AF221510S8	AF221517 Sus scrof
31	556.6	34.4	172674	80	AL359644	AL359644 Homo sapi
32	550.8	34.1	794	97	HUMGALOPS	J05421 Human 1,4-g
33	550.8	34.1	193168	62	AC011969	AC011969 Homo sapi
34	537.4	33.2	169269	70	AC026491	AC026491 Homo sapi
35	402	24.9	514	88	AF057428	AF057428 Cercocebu
36	402	24.9	514	88	AF057429	AF057429 Cercocebu
37	402	24.9	514	88	AF057430	AF057430 Cercocebu
38	400.4	24.8	514	88	AF057433	AF057433 Theropith
39	395.6	24.5	514	88	AF057432	AF057432 Papio sp.
40	394.6	24.4	514	88	AF057427	AF057427 Cercopith
41	394.6	24.4	514	88	AF057434	AF057434 Lophocebu
42	392.2	24.3	514	88	AF057435	AF057435 Lophocebu
43	390.8	24.2	514	88	AF057426	AF057426 Cercopith
44	378.8	23.4	505	88	AF057436	AF057436 Mandrillu
45	377.2	23.3	505	88	AF057431	AF057431 Mandrillu

ALIGNMENTS

```
RESULT   1
BOVGSTA
LOCUS       BOVGSTA       1828 bp    mRNA            MAM       27-APR-1993
DEFINITION  Bovine alpha 1,3 galactosyltransferase mRNA completed cds.
ACCESSION   J04989
VERSION     J04989.1  GI:164123
KEYWORDS    alpha-1,3 galactosyltransferase.
SOURCE      Bovine thymus, cDNA to mRNA, clone 41A.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 1828)
  AUTHORS   Joziasse,D.H., Shaper,J.H., Van den Eijnden,D.H., Van Tunen,A.J.
            and Shaper,N.L.
  TITLE     Bovine alpha 1,3 galactosyltransferase: isolation and
            characterization of a cDNA clone: identification of homologous
            sequences in human genomic DNA
  JOURNAL   J. Biol. Chem. 264, 14290-14297 (1989)
  MEDLINE   89340043
COMMENT     Draft entry and computer readable sequence for [1] kindly provided
            by D.H.Joziasse, 15 AUG 1989.
FEATURES             Location/Qualifiers
     source          1..1828
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
     mRNA            <1..1828
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                     /note="alpha 1-3 galactosyltransferase"
                     /codon_start=1
                     /protein_id="AAA30558.1"
                     /db_xref="GI:164124"
                     /translation="MNVKGKVILSMLVVSIVIVVFWEYIHSPEGSLFWINPSRNPEVG
                     GSSIQKGWWLPRWFNNGYHEEDGDINEEKEQRNEDESKLKLSDWFNPEKKPEVVTMTK
                     WKAPVVWEGTYNRAVLDNYYAKQKITVGLTVFAVGRYTEHYLEEFLTSANKHFMVGHP
                     VIFYIMVDDVSRMPLIELGPLRSFKVFKIKPEKRWQDISMMRMKTIGEHIVAHTQHEV
                     DFLFCMDVDQVFQDKFGVETLGESVAQLQAWWYKADPNDFTYERRKESAAYIPFGEGD
                     FYYHAAIFGGTPTQVLNITQECFKGILKDKKNDIEAQWHDESHLNKYFLLNKPTKLLS
                     PEYCWDYHIGLPADIKLVKMSWQTKEYNVVKNNV"
BASE COUNT       493 a    450 c    479 g    406 t
ORIGIN      144 bp upstream of BglI site.
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  Query Match          100.0%;  Score 1617;  DB 7;  Length 1828;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1617;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 ccgggggccgggccgagctgggagcggtcgagccccgctgcccagccgcccccgggctcccctc 60
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Db       1 ccgggggccgggccgagctgggagcggtcgagccccgctgcccagccgcccccgggctcccctc 60

Qy      61 gcgcccctgccgccgccgcccccgaggagcgccgccggccggccgacgggagccgccagccgc 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 gcgcccctgccgccgccgcccccgaggagcgccgccggccggccgacgggagccgccagccgc 120

Qy     121 acacccccgccccggcacgcccgcgggctcgggaggagcgcagccgccgcgactgttccggcc 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 acacccccgccccggcacgcccgcgggctcgggaggagcgcagccgccgcgactgttccggcc 180

Qy     181 agccgaggacgccgccccgggagccgagggcgccggccagccccagcgccgcccagcttctg 240
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Qy     241 cggatcaggggaaaccacgtgttcctcaagtggccagccagctgtcccccaagaggaacttgc 300
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Qy     301 ctgcgcatttgcacgggaaagacggagacacttcacaaaatcaacggagtccagaaggctgcac 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ctgcgcatttgcacgggaaagacggagacacttcacaaaatcaacggagtccagaaggctgcac 360

Qy     361 cttcgcttcctcccagccctgccgtcctctgtgcagaacggagctcagtagaaacttggtact 420
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Qy     421 tttgccttttactctaggaggagagaagcagacgatgaggagaaaataatgaatgtcaaa 480
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Qy     481 qqaaaaqtqattctgtcaatqctqqttqtctcaactgtcattgttgtgtttqqqaatat 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 ggaaaagtgattctgtcaatgctggttgtctcaactgtcattgttgtgtttgggaatat 540

Qy     541 atccacaqcccagaaggcictttgttctggataaacccatcaagaaacccagaagttggt 600
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Db     541 atccacagcccagaaggcictttgttctggataaacccatcaagaaacccagaagttggt 600

Qy     601 qqcaqcaqcattcaqaaqqqttqttqcttccqaqatqtttaacaatqttaccatqaa 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ggcagcagcattcagaaggqcttggtggcttccgagatggtttaacaatggttaccatgaa 660

Qy     661 qaaqatqqaqacataaacqaaqaaaaqgaacaaagaaacgaagacgaaagcaagcttaaq 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 gaagatggagacataaacgaagaaaaggaacaaagaaacgaagacgaaagcaagcttaag 720

Qy     721 ctatccqactqqttcaacccatttaaacqcccccaqqttqtqaccatqacqaaqtqqaaq 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 ctatcggactggttcaacccatttaaacgcccccaggttgtgaccatgacgaagtggaag 780

Qy     781 qctccaqtqqtqtqaqaaqqcictacqacaqaqccqtcttaqaraattattatqccaaq 840
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Db    781 GCTCCAGTGGTGTGGGAAGGCACTTACAACAGAGCCGTCTTAGACAATTATTATGCCAAG 840

Qy    841 cagaaaattaccgtcggcctgaccggttttcgcccgtcggaagatacattgagcattacttg 900
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Qy    901 gaggagttcttaacgtctgctaataaagcacttcatggtgggccacccagtcatcttttat 960
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Qy    961 atcatggtagatgatgtctccaggatgccttttgatagagttgggtcctctgcgctccttc 1020
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Qy   1021 aaagtgtttaagatcaagcctgagaagaggtggcaggacatcagcatgatgcgcatgaag 1080
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Qy   1201 cagctacaagcctggtggtacaaggcagatcccaatgacttcacctacgaggaggcggaag 1260
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Qy   1381 gacaagaaaaatgacataqaagcccaatggcatgatgaaagccatctaaacaagtatttc 1440
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RESULT   2
AR066334
LOCUS       AR066334     1828 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 8 from patent US 5849991.
ACCESSION   AR066334
VERSION     AR066334.1  GI:5996550
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1828)
  AUTHORS   d'Apice,A.J.F., Pearse,M.J., Robins,A.J., Crawford,R.J. and
            Rathjen,P.D.
  TITLE     Mice homozygous for an inactivated .alpha. 1,3-galactosyl
            transferase gene
  JOURNAL   Patent: US 5849991-A 8 15-DEC-1998;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT      493 a    450 c    479 g    406 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1617;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CCGGGGGCCGGGCCGAGCTGGGAGCGTCGAGCCCGCTGCCCAGCGCCCGCCGGCTCCCTC 60

Qy      61 gcgccccctgcccgccgccccccgaggaggcgccccggcgggccggccgacgggagccgcagccggc 120
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Qy     121 acaccccgccccggcacgcccgcgggggctcgggaggaggcagcgccgccgactgttccggc 180
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Qy     181 agccgaggacgccgccgggagccgaggcgccggccagccccccagcgcgccccagcttctg 240
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Qy     241 cggatcagggaaaccacgtgtcctcaagtggccagccagctgtccccaagaggaagcttggc 300
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Qy     301 ctggcatttgcacggaaagacgagacacttcacaaaatcaacggagtcagaagctgcac 360
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Qy     361 cttcgcttcctcccagccctgcctccttctgcagaacggagctcagtagaacttggtact 420
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Qy     421 tttgccttttactctaggaggagagaagcagacgatgaggagaaaattaatgaatgtcaaa 480
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Qy     481 ggaaaagtgattctgtcaatgctggttgtctcaactgtcattgttgtgttttgggaatat 540
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Qy     781 gctccagtggtgtgggaagggcacttacaacagagccgtcttagacaattattatgccaag 840
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Db     781 GCTCCAGTGGTGTGGGAAGGCACTTACAACAGAGCCGTCTTAGACAATTATTATGCCAAG 840

Qy     841 cagaaaattaccgtcggcctgaccggttttcgcccgtcggaagatacattgagcattacttg 900
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Db     841 CAGAAAATTACCGTCGGCCTGACGGTTTTCGCCCGTCGGAAGATACATTGAGCATTACTTG 900

Qy     901 gaggagttcttaacgtctgctaataaagcacttcatggtgggccacccagtcatcttttat 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GAGGAGTTCTTAACGTCTGCTAATAAGCACTTCATGGTGGGCCACCCAGTCATCTTTTAT 960
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Qy      961 atcatqqtaqatqatqtqtctccaqqatqcctttqataqaqttqqqtcctctqcqctcctc 1020
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Db      961 ATCATGGTACATGATGTTCTCCAGGATGCCTTTGATAGAGTTGGGTCCTCTGCGCTCCTTC 1020

Qy     1021 aaaqtqtttaaqatcaaqcctqaqaaaqaqttqqcaqqacatcaqcatqatqatqcqcatqaaq 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 AAAGTGTTTAACATCAAGCCTGAGAAGAGGTGGCACGACATCAGCATGATGCGCATGAAG 1080

Qy     1081 actatcqqqqaqcacatttqtqqcccacatccaqcatqaqqttqacttcctttttctqcatq 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 ACTATCGGGGAGCACATTGTGGCCCACATCCAGCATGAGGTTGACTTCCTTTTCTGCATG 1140

Qy     1141 qatqtqqacccaqqtctttccaaqacaaqttttqqqqtqqaqacccctqqqcqaqtcqqtqqcc 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 GATGTGGACCCAGGTCTTCCAAGACAAGTTTGGGGTGGAGACCCTGGGCGAGTCGGTGGCC 1200

Qy     1201 cqqctacaaqcctqqtqqtacqaqqcaqatcccaatqacttcacctacqacqaqqcqqaaq 1260
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Db     1201 CAGCTACAAGCCTGGTGGTACGAGGCAGATCCCAATGACTTCACCTACGACGAGGCGGAAG 1260

Qy     1261 qaqtctqcaqcatacatttcccttcqqcqaaqqqqatttttattaccatqcaqccatttttt 1320
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Db     1261 GAGTCTGCAGCATACATTCCCTTCGGCGAAGGGGATTTTTATTACCATGCAGCCATTTTT 1320

Qy     1321 qqqqaaacacccactcaqqtcctttaacatcaccccaqqaatqcttcaaaqqaatcctcaaq 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 GGGGCAACACCCACTCAGGTCCTTAACATCACCCAGGAATGCTTCAAAGGAATCCTCAAG 1380

Qy     1381 qacaaqqaaaatqacataqaaqcccaatqqcatqatqaaaqccatctaaacaaqtatttc 1440
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Qy     1441 cttctcaacaaacctactaaaatcttatccccqqaatactqctqqqattatcacatagqc 1500
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Db     1441 CTTCTCAACAAACCTACTAAAATCTTATCCCCGGAATACTGCTGGGATTATCACATAGGC 1500

Qy     1501 ctacctqccqqatattaaqcttqtcaaqatqtcttqqcaqacaaaaqaqtataatqtqqtt 1560
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Db     1501 CTACCTGCCGGATATTAAGCTTGTCAAGATGTCTTGGCAGACAAAAGAGTATAATGTGGTT 1560

Qy     1561 aqaaataatqtctcqacttqtqccaqtacatttctqaatttqaqaqaqtattattct 1617
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RESULT  3
AF221508
LOCUS       AF221508      3684 bp    mRNA            MAM       04 FEB-2001
DEFINITION  Sus scrota clone A alpha 1,3-galactosyltransferase mRNA, complete
            cds, alternatively spliced.
ACCESSION   AF221508
VERSION     AF221508.1  GI:12658440
KEYWORDS    .
SOURCE      pig.
  ORGANISM  Sus scrota
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 3684)
  AUTHORS   Koike,C., Friday,R.P., Nakashima,I., Luppi,P., Funq,J.J., Rao,A.S.,
            Starzl,T.E. and Trucco,M.
  TITLE     Isolation of the regulatory regions and genomic organization of the
            porcine alpha1,3 galactosyltransferase gene
  JOURNAL   Transplantation 70 (9), 1275-1283 (2000)
  MEDLINE   20537976
   PUBMED   11087141
REFERENCE   2  (bases 1 to 3684)
  AUTHORS   Koike,C., Friday,R.P., Libert,T., Protozich,J., Nakashima,I.,
            Luppi,P., Funq,J.J., Rao,A.S., Starzl,T.E. and Trucco,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (23 JAN 2001) Surgery, University of Pittsburgh, 3601
            Fifth Avenue, Falk Clinic 4th Floor, Pittsburgh, PA 15213, USA
FEATURES             Location/Qualifiers
     source          1..3684
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                     /clone="A"
     CDS             676..1791
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                     /codon_start=1
                     /product="alpha 1,3-galactosyltransferase"
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                     /db_xref="GI:12658441"
                     /translation="MNVKGKVVLSMLLVSTVMVVFWEYINSPEGSLFWIYQSKNPEVG
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                     TTRWKAPVVWEGTYNRAVLDNYYAKQKITVGLTVFAVGRYTEHYLEEFLISANTYFMV
                     GHKVIFYTMVDDISRMPLIELGPLRSEKVFETKSEKRWQDISMMRMKFIGEHILAHIQ
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                     QGDFYYHAAIFGGTPTQVLNITQECFKGIQDKENDIEAEWHDESHLNKYFLLNKPTK
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BASE COUNT     1041 a    854 c    873 g    916 t
ORIGIN
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  Query Match             62.2%;  Score 1005;  DB 7;  Length 4684;
  Best Local Similarity   81.5%;  Pred. No. 1.6e-196;
  Matches 1389;  Conservative    0;  Mismatches  175;  Indels  129;  Gaps   10;

Qy        1 ccqqqqqcccqqqccqaqctqqqaqcqtccqacccqctqcccaqccqcccqccqqqctcccctc 60
            ||| |||||||| |||| |||||| |||||| |||||| |||||||||||| ||||
Db      299 CCGCGGGCCCGGGTGGAGCGGGGAGCTCCGCCGCCCGCCGCCCCAGTGCCCGCCGGCTCCTC 458

Qy       61 qcqcccctqcccqcccqcccqaaqaqcqcccqqcqacccqccqcaqqqaqcqca-qcqq 119
            |||||||||||||| |||||||||||| | | |||||||| | | |||||||| ||||
Db      359 GCGCCCTGCCCCGCCACCCCGGAGGAGCACACAGCGGCCCGGCGGGCCGGAGCGCAGGCGG 418

Qy      120 cacacccqcccccqqcacqccc-qcqqqqctcqqqaqqqaqqcaqcqcqccqcactqttccq 178
            |||||||||||||||||||||| || | |||| |||| | || ||||||| ||||||||
Db      419 CACACCCGCGCCCGGCACGCCCTGCCGAGCTCAGGAGCACGCCGCGCGGC-ACTGTTCGC 477

Qy      179 qcaqccqaqqacqcccqccq-------qqqaqccqaqqcqccqqcccaqcccccaqcqcqcc 231
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Db      478 TCAGCCGAGGACGCCGCCGGGGGGGCCGGGAGCCGAGGTGTGGGCCATCCCCGAGCGCACC 537

Qy      232 caqcttctqcqqatcaqqqaaaccacqtqtcctcaaqtqqccaqccaqcaqctqtccccaaqa 291
            |||||||||| |||||
Db      538 CAGCTTCTGCCGATCA-- ------- ------  -----  ---  ------- -- 553

Qy      292 qqaacttqcctqqcattqcacqqaaaqacqaqaacacttcacaaaatcaaccqqaqtcaqa 351
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Db      554 ------------------- ------------ ------- ---GGAGTTGGA 562

Qy      352 aqqctqcacctteqcttcctcccaqccctqcctcctctqcaqaacqqaqctcaqtaqaa 411
            | || |||||||| |||||||||||||||||||||||||| | |||||| ||||
Db      563 ACGCAGCACCTTCCCTTCCTCCCAGCCCTGCCTCCTTCTGCAGAGCAGAGCTCACTAGAA 622

Qy      412 cttqqtacttttqccttttacttctaqqaqqaqaaaacaqacqatqaqqaqaaaataatq 471
            ||||   ||| |||||||||||| || |||||||||||| ||||||||||||||||||
Db      623 CTTG----TTTCGCCTTTTACTCTGGGGGGAGAGAAGCAGAGGATGAGGAGAAAATAATG 678

Qy      472 aatqtcaaaqqaaaaqtqattctqtcaatqctqqttqtctcaactqtcattqttqtqttt 531
            |||||||||||| |||| |||||||||||| |||||||||||| || ||||||||||
Db      679 AATGTCAAAGGAAGAGTGGTTCTGTCAATGCTGCTTGTCTCAACTGTAATGGTTGTGTTT 738

Qy      532 tqqqaatatatcccacaqcccaqaaqqctctttqttctqqataaacccatcaaqaaacccq 591
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Db      739 TGGGAATACATCAACAGCCCAGAAGGTTCTTTGTTCTGGATATACCAGTCAAAAACCCA 798

Qy      592 qaaqttqqtqqcaqcaqcaqcattcaqaaqqqctqqtqqcttcccaqaatqqttttaacaatq-- 649
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Db      799 GAAGT---TCGCAGCAGTGCTCACAGGGGCTGGTGGTTTCCGAGCTGGTTTAACAATGGG 855

Qy      650 ------qttaccatqaaqaaqatqqaqacataaacqaaqaaaaaaqqqacqaaqaaacqaa 702
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Db      856 ACTCACAGTTACCACGAAGAAGAAGACGCTATAGGCAACGAAAAGGAACAAAGAAAAGAA 915

Qy      703 qacqa---aaqcaaqcttaaqctatcqqactqqttcaaccqatttaaacqccccqaqqtt 759
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Db    916 GACAACAGAGGAGAGCTTCCGCTAGTGGACTGGTTTAATCCTGAGAAACGCCCAGAGGTC 975

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Db    976 GTGACCATAACCAGATGGAAGGCTCCAGTGGTATGGCAAGGCACTTACAACAGAGCCGTC 1035

Qy    820 ttagacaattattatgccaagcagaaaattaccgtcggcctgacggttttcgccgtcgga 879
Db   1036 TTAGATAATTATTATGCCAAACAGAAAATTACCGTGGGCTTGACGGTTTTTGCTGTCGGA 1095

Qy    880 agatacattgaagcattacttggaggaagttcttaacgtctgctaataaqcacttcatggtg 939
Db   1096 AGATACATTGAGCATTACTTGGAGGAGTTCTTAATATCTGCAAATACATACTTCATGGTT 1155

Qy    940 ggccacccaqtcatcttttatatcatggtagatgatgtctccaggatgccttttgatagaq 999
Db   1156 GGCCACAAAGTCATCTTTTACATCATGGTGGATGATATCTCCAGGATGCCTTTGATAGAG 1215

Qy   1000 ttgggtcctctgcgctccttcaaaqtgtttaagatcaagcctgagaaqaqqtqqcaggac 1059
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Qy   1060 atcagcatgatgcggcatgaagacatcggggagcacatcctggcccacatccagcacgag 1119
Db   1276 ATCAGCATGATGCGGCATGAAGACATCGGGGAGCACATCCTGGCCCACATCCAGCACGAG 1335

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Db   1336 GTGGACTTCCTCTTCTGCATGGACGTGGATCAGGTCTTCCAAAACAACTTTGGGGTGGAG 1395

Qy   1180 accctgggcgagtcggtggcccagctacaagcctggtggtacaaggcagatcccaatgac 1239
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Db   1456 TTCACCTACGAGAGGCGGAAGGAGTCCGCAGCCTACATTCCGTTTGGCCAGGGGGATTTT 1515

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Qy   1540 acaaaagaqtataatgtggttagaaataatgtctgact-----ttgtgccagtacatttc 1594
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Qy   1595 tgaatttgagagagtattattct 1617
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RESULT  4
AF221509
LOCUS       AF221509     3640 bp    mRNA            MAM       04-FEB-2001
DEFINITION  Sus scrofa clone B alpha-1,3-galactosyltransferase mRNA, complete
            cds, alternatively spliced.
ACCESSION   AF221509
VERSION     AF221509.1  GI:12658442
KEYWORDS    .
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 3640)
  AUTHORS   Koike,C., Friday,R.P., Nakashima,I., Luppi,P., Fung,J.J., Rao,A.S.,
            Starzl,T.E. and Trucco,M.
  TITLE     Isolation of the regulatory regions and genomic organization of the
            porcine alpha1,3-galactosyltransferase gene
  JOURNAL   Transplantation 70 (9), 1275-1285 (2000)
  MEDLINE   20537976
   PUBMED   11087141
REFERENCE   2  (bases 1 to 3640)
  AUTHORS   Koike,C., Friday,R.P., Libert,T., Profozich,J., Nakashima,I.,
            Luppi,P., Fung,J.J., Rao,A.S., Starzl,T.E. and Trucco,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JAN-2001) Surgery, University of Pittsburgh, 3601
            Fifth Avenue, Falk Clinic 4th Floor, Pittsburgh, PA 15213, USA
FEATURES             Location/Qualifiers
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ORIGIN


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  Best Local Similarity   87.0%;  Pred. No. 4.9e-189;
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Qy    398 ggagctcagtagaaacttggtactttqcctttactctaqqaqgaqaaaaqcaqacqatg 457
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Qy    458 aggagaaaataatgaatgtcaaaqqaaaaqtgattctatcaatgctgattgtctcaactg 517
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Qy    518 tcattgttgtgttttqqgaatatatccacaqcccagaaqqctctttgttctgatagaacc 577
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Qy    578 catcaagaaacccagaagttggtggcagcagcattcagaaggqgctgttggcttccgaaat 637
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Qy    638 gqtttaacaatg---------qttaccatqaaqaaqatqqaqacatgaacqaaqaaaaaq 688
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Qy    689 aacaaagaaacqaaqacqa---aaqcaaqcttaaqctatcqqactqqttcaacccatttta 745
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Qy    746 aacgcccgaggttgtgaccatgacgaagtggaaggctccagtggtgtgggaaggcacttt 805
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Qy    986 tqccttqataqaqttqqqtcctctqcqctccttcaaaqtqtttaaqatcaaqcctqaqa 1045
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Qy   1106 acatccaqcatqaqqttqacttcctttttctqcatqqatqtqqaccaqqtcttccaaqaca 1165
Db   1278 ACATCCAGCACGAGGTGGACTTCGTCTTCTGCATGGACGTGGATCAGGTCTTCCAAAACA 1337

Qy   1166 aqttqqqqtqqaqaccctqqqcqaqtcqqtqqcccaqctacaaqcctqatqqtacaaqg 1225
Db   1338 ACTTTGGGCTGGAGACCCTGGGCCAGTCGGTGGCTCAGCTACAGGCCTGGTGGTACAAGG 1397

Qy   1226 cagatcccaatqacttcacctacqaqaqqcqqaaqqaqtctqcaqcatacattcccttcq 1285
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Db   1698 AGATAGCTTGGCAGAAAAAAGAGTATAATTTGGTTAGAAATAACATCTGACTTTAAATTG 1757

Qy   1581 tqccaqtacatttctqaatttqaqaqaqtattatlct 1617
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RESULT    5
AR066433
LOCUS       AR066433      1412 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 7 from patent US 5849991.
ACCESSION   AR066433
VERSION     AR066433.1  GI:5996549
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1412)
  AUTHORS   d'Apice,A.J.F., Pearse,M.J., Robins,A.J., Crawford,R.J. and
            Rathjen,P.D.
  TITLE     Mice homozygous for an inactivated .alpha. 1,3-galactosyl
            transferase gene
  JOURNAL   Patent: US 5849991-A 7 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1..1412
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BASE COUNT      419 a    290 c    444 g    459 t
ORIGIN


  Query Match           58.4%;  Score 944.4;  DB 9;  Length 1412;
  Best Local Similarity  87.3%;  Pred. No. 5.2e-184;
  Matches 1100;  Conservative    0;  Mismatches  136;  Indels   24;  Gaps    5;

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Qy    435 taqqaqqaqaqaaqcaqacqatqacqaqqaqaaaataatqaatqtctaaaqqaaaaqtqattct 494
Db     57 TGCGGGGAGACAAGCAGACGATGACGCAGAAAATAATGAATGTCAAAGGAAGAGTCGTTCT 116

Qy    495 qtcaatqctqqttqtctcaactqtcattqttqtqttttqqqaatatatcccacaqcccaqa 554
Db    117 GTCAATGCTGCTTGTCTCAACTGTAATGGTTGTGTTTTGGGAATACATCAACAGCCCAGA 176

Qy    555 aqqctctttqttctqqataaacccatcaaqaaacccaaaaqttqqtqqcaqcaqcattca 614
Db    177 AGGTTCTTTGTTCTGGATATACCAGTCAAAAAACCCAGAAGT---TGGCAGCAGTGCTCA 233

Qy    615 qaaqqqtqqtqqcttccqaqatqatttaacaatq---------qttaccatqaaqaaqa 665
Db    234 GAGGGCTGGTGGTTTCCGAGCTGGTTTAACAATGGGACTCACAGTTACCACGAAGAAGA 293

Qy    666 tqqaqacatqaacqaaqaaaaqqaacaaaqaaacqaaqacqa---aaqcaaqcttaaqct 722
Db    294 AGACGCTATAGGCAACGAAAAGGAACAAAGAAAAGAAGACAACAGAGGAGAGCTTCCGCT 353

Qy    723 atcqqactqqttcaaccctttaaacqccccqaqqttqtqaccatqacqaaqtqqaaqqc 782
Db    354 AGTGGACTGGTTTAATCCTGAGAAACGCCCAGAGGTCGTGACCATAACCAGATGGAAGGC 413

Qy    783 tccatqqtqtqqqaaqqcacttacaacaqaqccqtcttaqacaattattatqccaaqca 842
Db    414 TCCAGTGGTATGGGAAGGCACTTACAACAGAGCCGTCTTAGATAATTATTATGCCAAACA 473

Qy    843 qaaaattaccqtcqqcctqacqqtttcqcccqtcqqaaqatacattqaqcattacttqqa 902
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Qy    963 catqqtaqatqatqtctcccaqqatqccttqatagaqttqqqtcctctqcqctccttcaa 1022
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Qy   1083 tatcqqqqaqcacattqtqqcccacatccaqcatqaqqttqacttcctttttctqcatqqa 1142
Db    714 CATCGGGGAGCACATCGTGGCCCACATCCAGCACGAGGTGGACTTCGTCTTCTGCATGGA 773

Qy   1143 tqtqqaccaqgtcttccaaqacaaqtttqqqqtqqaqaccctqqqcqaqtcqqtqqcccca 1202
Db    774 CGTGGATCAGGTCTTCCAAAACAACTTTGGGGTGGAGACCCTGGGCCAGTCGGTGGCTCA 833

Qy   1203 qctacaaqcctqatqqtacaaqqcagatcccaatqacttcacctacqaqaqqcqqaaqga 1262
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Qy   1263 gtctgcagcatacattcccttcggcgaaggggattttattaccatgcagccatttttgg 1322
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Qy   1323 gggaacacccactcaggtcttaacatcacccaggaatgcttcaaaggaaatcctcaaagga 1382
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Qy   1383 caagaaaaatgacatagaagccgaatggcatgatgaaagccatctaaacaagtatttcct 1442
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Qy   1443 tctcaacaaacctactaaaatcttatccccggaatactgctgggattatcacatagggcct 1502
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Db   1074 TCTCAACAAACCCACTAAAATCTTATCCCCAGAATACTGCTGGGATTATCATATAGGCAT 1133

Qy   1503 acctgcggatattaagcttgtcaagatgtcttggcagacaaaaagagtataatgtggttag 1562
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Qy   1563 aaataatgtctgact-----ttgtgccagtacatttctgaatttgagagagagtattattct 1617
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DEFINITION  Sus scrofa alpha-1,3-galactosyltransferase mRNA, complete cds.
ACCESSION   L36152
VERSION     L36152.1  GI:642635
KEYWORDS    alpha-1,3-galactosyltransferase.
SOURCE      Sus scrofa.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 1269)
  AUTHORS   Strahan,K.M., Gu,F., Preece,A.F., Gustavsson,I., Andersson,L. and
            Gustafsson,K.
  TITLE     cDNA sequence and chromosome localization of pig alpha 1,3
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  JOURNAL   Immunogenetics 41 (2-3), 101-105 (1995)
  MEDLINE   95104914
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                     QGDFYYHAAIFGGTPTQVLNITQECFKGILQDKENDIEAEWHDESHLNKYFLLNKPIK
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Db     62 CTGTAATGGTTGTGTTTTGGGAATACATCAACAGCCCAGAAGGTTCTTTGTTCTGGATAT 121

Qy    575 acccatcaagaaacccagaagttggtggcagcagcattcagaaaggctgttggcttccga 634
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Db    122 ACCAGTCAAAAAACCCAGAAGT---TGGCAGCAGTGCTCAGAGGGGCTGGTGGTTTCCGA 178

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Db    359 CTTACAACAGAGCCGTCTTAGATAATTATTATGCCAAACAGAAAATTACCGTGGGCTTGA 418

Qy    863 cggttttcgccgtcggaaagatacattgagcattacttggaggaagttcttaacgtctgcta 922
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Db    419 CGGTTTTTGCTGTCGGAAGATACATTGAGCATTACTTGGAGGAGTTCTTAATATCTGCAA 478

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Qy    983 ggatgccttttgataagagttgggtcctctgcgctccttcaaagtgtttaagatcaagcctg 1042
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Db    539 GGATGCCTTTGATAGAGCTGGGTCCTCTGCGTTCCTTTAAAGTGTTGAGATCAAGTCCG 598

Qy   1043 agaagaggtggcaggacatcagcatgatgcgcatgaagactatcgggggagcacattgtgg 1102
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Db    719 ACAACTTTGGGGTGGAGACCCTGGGCCAGTCGGTGGCTCAGCTACAGGCCTGGTGGTACA 778

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Db    779 AGGCACATCCTGACGAGTTCACCTACGAGAGGCGGAAGGAGTCCGCAGCCTACATTCCGT 838

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Db    839 TTGGCCAGGGGGATTTTTATTACCACGCAGCCATTTTTGGGGGAACACCCACTCAGGTTC 898

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Db   1019 TCTTATCCCCAGAATACTGCTGGGATTATCATATAGGCATGTCTGTGGATATTAGGATTG 1078

Qy   1523 tcaagatgtcttggcagacaaaaagagtataatgtggttagaaaataatgtctgact----- 1577
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Db    1079 TCAAGATAGCTTGGCAGAAAAAACAGTATAATTTGGTTAGAAATAACATCTGACTTTAAA 1138

Qy    1578 ttqtqccaqtacatttctqaatttqaaaqaqtattattct 1617
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Db    1139 TTGTGCCAGCAGTTTTCTGAATTTGAAAGAGTATTACTCT 1178


RESULT   7
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LOCUS       A69444         1128 bp    DNA              PAT        06-MAY-1999
DEFINITION  Sequence 1 from Patent WO9802453.
ACCESSION   A69444
VERSION     A69444.1  GI:4760171
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1128)
  AUTHORS   Gomlet,P., Robberecht,P., Vandermeers,A. and Woelbroeck,M.
  TITLE     PEPTIDIC LIGANDS HAVING A HIGHER SELECTIVITY FOR THE VIP1 RECEPTOR
            THAN FOR THE VIP2 RECEPTOR
  JOURNAL   Patent: WO 9802453-A 1 22-JAN-1998;
            UNIV BRUXELLES (BE)
FEATURES             Location/Qualifiers
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BASE COUNT       335 a     236 c     286 g     271 t
ORIGIN


  Query Match          54.6%;  Score 866;  DB 9;  Length 1128;
  Best Local Similarity   87.6%;  Pred. No. 6.9e-168;
  Matches  986;  Conservative    0;  Mismatches  125;  Indels   15;  Gaps    3;

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Qy     642 taacaatq      ----qttaccatqaaqaaqatqqaqacataaacqaaqaaaaqqaaca 692
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Qy     693 aaqaaacqaaqaqa    aaqcaaqcttaaqctataqqactqttcaaccattttaaacq 749
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Qy     810 caqaqccqtctttqaqacaattattatqccaaqcaqaaaattaccqtcqqcctqacqqttttt 869
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Db     363 CAGAGCCGTCTTAGATAATTATTATGCCAAACAGAAAATTACCGTGGGCTTGACGGTTCT 422

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Qy     930 cttcatqqtqqqccacccaqtcatctttttatatcatqqtaqatqtatqtctcccaqaatqcc 989
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Db     483 CTTCATGGTTGGCCACAAAGTCATCTTTTACATCATGGTGGATGATATCTCCAGCATGCC 542

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RESULT   8
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DEFINITION  Sequence 1 from Patent WO9803653.
ACCESSION   A72021
VERSION     A72021.1  GI:4808047
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1128)
  AUTHORS   Pourcel,C., Soulillou,J. and Vanhove,B.
  TITLE     METHOD FOR PREPARING TRANSGENIC NON-HUMAN MAMMALIAN ORGANS FOR
            TRANSPLANTATION TO HUMANS, AND NUCLEOTIDE SEQUENCES THEREFOR
  JOURNAL   Patent: WO 9803653-A 1 29-JAN-1998;
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COMMENT     Other publication FR 2751346 19980123.
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BASE COUNT       335 a    236 c    286 g    271 t
ORIGIN


  Query Match           53.6%;  Score 866;  DB 9;  Length 1128;
  Best Local Similarity   87.6%;  Pred. No. 6.9e-168;
  Matches  986;  Conservative    0;  Mismatches  125;  Indels   15;  Gaps    3;

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Db     303 CCCAGAGGTCGTGACCATAACCAGATGGAAGGCTCCAGTGGTATGGGAAGGCACTTACAA 362

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Db     723 TGGGGTGGAGACCCTGGGCCAGTCGGTGGCTCAGCTACAGGCCTGGTGGTACAAGGCACA 782

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Db     783 ICCTGACGAGTTCACCTACGAGAGGCGGAAGGAGTCCGCAGCCTACATTCCGTTTGGCCA 842

Qy    1290 aqqggattttattaccatgcagccatttttqqqqqaacacccactcaqqtcctaacat 1349
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DEFINITION  alpha 1,3 galactosyltransferase [New World monkeys, marmoset
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ACCESSION   S71333
VERSION     S71333.1  GI:558051
KEYWORDS    .
SOURCE      New World monkeys.
  ORGANISM  Platyrrhini
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            Mammalia; Eutheria; Primates.
REFERENCE   1  (bases 1 to 1131)
  AUTHORS   Henion,T.R., Macher,B.A., Anaraki,F. and Galili,U.
  TITLE     Defining the minimal size of catalytically active primate alpha 1,3
            galactosyltransferase: structure-function studies on the
            recombinant truncated enzyme
  JOURNAL   Glycobiology 4 (2), 193-201 (1994)
  MEDLINE   94331837
  REMARK    GenBank staff at the National Library of Medicine created this
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            This sequence comes from Fig. 1.
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ORIGIN


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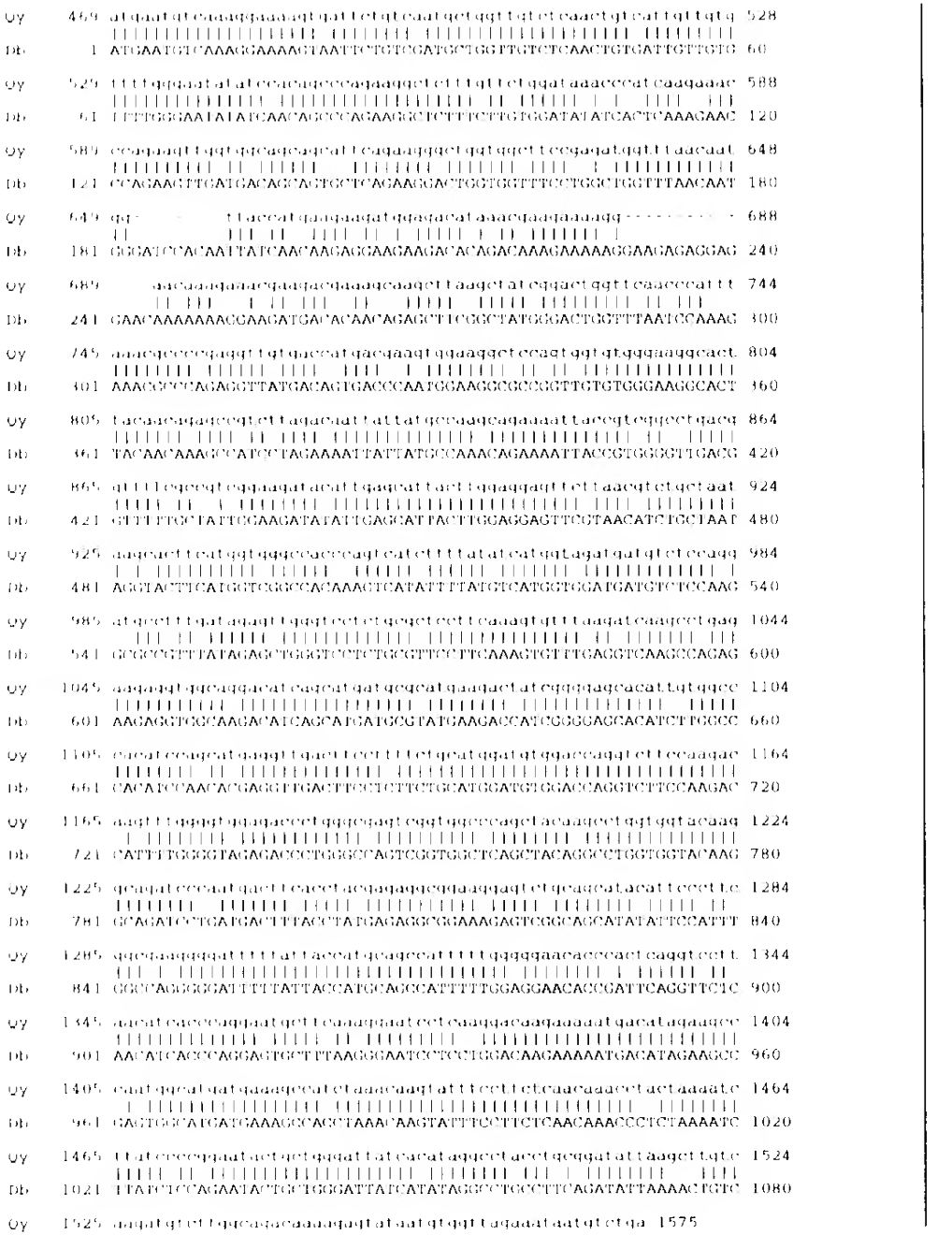

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DEFINITION  Sus scrofa (clone pPGT-3) alpha 1,3-galactosyltransferase mRNA,
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ACCESSION   L36535
VERSION     L36535.1  GI:609566
KEYWORDS    alpha-1,3-galactosyltransferase.
SOURCE      Sus scrofa spleen and liver cDNA to mRNA.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 1343)
  AUTHORS   Sandrin,M.S., Dabkowski,P.L., Henning,M.M., Moulton,E. and
            McKenzie,I.F.C.
  TITLE     Characterization of cDNA clones for porcine a(1,3)galactosyl
            transferase: The enzyme generating the Gala(1,3)Gal epitope
  JOURNAL   Xenotransplantation (1994) In press
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Qy   504 gttgtctcaactgtcattgttgtgttttgggaatatatccacagcccagaaggctctttg 563
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Qy     972 tqatqtctccaqqatqccttttqataqaqttgggtcctctqcqctccttcaaaqtqtttaa 1031
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RESULT 11
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VERSION     AR048516.1  GI:5970859
KEYWORDS    .
SOURCE      Unknown
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1423)
  AUTHORS   Sandrin,M.S. and McKenzie,I.F.C.
  TITLE     Xenotransplantation therapies
  JOURNAL   Patent: US 5821117-A 2 13-OCT-1998;
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RESULT  12
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LOCUS       A69346        1092 bp    DNA             PAT       06-MAY-1999
DEFINITION  Sequence 4 from Patent WO9802453.
ACCESSION   A69346
VERSION     A69346.1  GI:4760174
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1092)
  AUTHORS   Gourlet,P., Robberecht,P., Vandermeers,A. and Woelbroeck,M.
  TITLE     PEPTIDIC LIGANDS HAVING A HIGHER SELECTIVITY FOR THE VIP1 RECEPTOR
            THAN FOR THE VIP2 RECEPTOR
  JOURNAL   Patent: WO 9802453 A 4 22 JAN 1998;
            UNIV BRUXELLES (BE)
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BASE COUNT       325 a    228 c    279 g    260 t
ORIGIN


  Query Match             49.0%;  Score 792;  DB 9;  Length 1092;
  Best Local Similarity   84.8%;  Pred. No. 1.1e-152;
  Matches  956;  Conservative    0;  Mismatches  120;  Indels   51;  Gaps    4;

Qy     462 qaaaataatqaatqtctcaaaqqaaaaqtqattctqtcaatqctqqttqtctcaactqtcat 521
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RESULT  13
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LOCUS       A72023        1092 bp    DNA             PAT       11-MAY-1999
DEFINITION  Sequence 3 from Patent WO9803654.
ACCESSION   A72023
VERSION     A72023.1  GI:4808049
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
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            unclassified.
REFERENCE   1  (bases 1 to 1092)
  AUTHORS   Pourcel,C., Soulillou,J. and Vanhove,B.
  TITLE     METHOD FOR PREPARING TRANSGENIC NON-HUMAN MAMMALIAN ORGANS FOR
            TRANSPLANTATION TO HUMANS, AND NUCLEOTIDE SEQUENCES THEREFOR
  JOURNAL   Patent: WO 9803653-A 29-JAN-1998;
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COMMENT     Other publication FR 2751346 19980123.
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ORIGIN


  Query Match             49.0%;  Score 792;  DB 9;  Length 1092;
  Best Local Similarity   84.8%;  Pred. No. 1.1e-152;
  Matches  955;  Conservative    0;  Mismatches  120;  Indels   51;  Gaps    4;

Qy     462 qaaaataatqaatqtcaaaqqaaaaqtqattctqtcaatqctqqttqtctcaactqtcat 521
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RESULT  14
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DEFINITION  Sequence 5 from Patent WO9802453.
ACCESSION   A69348
VERSION     A69348.1  GI:4760175
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1065)
  AUTHORS   Gourlet,P., Robberecht,P., Vandermeers,A. and Woolbroeck,M.
  TITLE     PEPTIDIC LIGANDS HAVING A HIGHER SELECTIVITY FOR THE VIP1 RECEPTOR
            THAN FOR THE VIP2 RECEPTOR
  JOURNAL   Patent: WO 9802453-A 5 22-JAN-1998;
            UNIV BRUXELLES (BE)
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VERSION     A72025.1  GI:4808051
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1065)
  AUTHORS   Pourcel,C., Soulillou,J. and Vanhove,B.
  TITLE     METHOD FOR PREPARING TRANSGENIC NON-HUMAN MAMMALIAN ORGANS FOR
            TRANSPLANTATION TO HUMANS, AND NUCLEOTIDE SEQUENCES THEREFOR
  JOURNAL   Patent: WO 9803658 A 29-JAN-1998;
            INST NAT SANTE RECH MED (FR)
COMMENT     Other publication FR 2751846 19980123.
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ORIGIN


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